SEQUENCE LISTING

<110> MASTERNAK, Krzysztof
REITH, Walter
MACH, Bernard

<120> New Transcription Factors of MHC Class II Genes, Substances Capable of Inhibiting This New Transcription Factor and Medical Uses of These Substances

<130> 010830-117

<140> US 09/840,243
<141> 2001-04-24

<150> EP 98120085.0
<151> 1998-10-24

<160> 22

<170> PatentIn Ver. 2.1

<210> 1
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 1
ccgtacgcgt ctagaccatg gagcttaccc agcctgcaga 40

<210> 2
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 2
ttcgaattct cgagtgtctg agtccccggc a 31

<210> 3
<211> 37
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 3
ccgtacgcgt ctagaccatg gagcccactc aggttgc 37

<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
ttcgaattct cgagtgcctg ggttccagca gg 32

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
ccagctctag actccaccac tctcaccaac 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 6
ccttcgaatt ctcgctcttt tgccaggatg 30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 7
ggttctctag attggcagca ctggggatag 30

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
gctacgaatt ccagcagaca cagccaaaac 30

<210> 9
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct tacccagcct 60

gcagaagac 69

<210> 10
<211> 1345
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (418)..(1200)

<400> 10
acgcagggaa ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60

ggctggtgga gcgacaccca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120

cttttccttg agagacgagt tgggggagtc ctccacgcat tacccactcg ggccgcaaaa 180

actcccttct ttagccctct gcccccgccc ttgcttataa gcctttgaga ccgcagaagg 240

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gaccttgttg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300

gtttgcctcc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360

gagagaactg ggctttcggc gcgggggggac agaggaggct cgtggggagc tttcccc    417

atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc   465
Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
  1               5                  10                  15

cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca   513
Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
             20                  25                  30

gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag   561
Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
         35                  40                  45

cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc   609
Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
     50                  55                  60

agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac   657
Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65                  70                  75                  80

gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag   705
Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
                 85                  90                  95

ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa   753
Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
            100                 105                 110

ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc   801
Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
        115                 120                 125

atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg   849
Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
    130                 135                 140

gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc   897
Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
145                 150                 155                 160

ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg   945
Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
                165                 170                 175
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ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg   993
Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
            180                 185                 190

cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc   1041
Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
        195                 200                 205

ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac   1089
Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
    210                 215                 220

acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag   1137
Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
225                 230                 235                 240

gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc   1185
Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
                245                 250                 255

gct gac cct gag tga aggccgcctg ccggggactc agacactcag ggaacaaaat   1240
Ala Asp Pro Glu
            260

ggtcagccag agctggggaa acccagaact gacttcaaag gcagcttctg gacaggtggt 1300

gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag                1345


<210> 11
<211> 260
<212> PRT
<213> Homo sapiens

<400> 11
Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
  1               5                  10                  15

Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
             20                  25                  30

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
         35                  40                  45

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
     50                  55                  60

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
 65                  70                  75                  80
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Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
                 85                  90                  95

Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
            100                 105                 110

Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
        115                 120                 125

Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
    130                 135                 140

Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
145                 150                 155                 160

Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
                165                 170                 175

Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
            180                 185                 190

Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
        195                 200                 205

Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
    210                 215                 220

Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
225                 230                 235                 240

Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
                245                 250                 255

Ala Asp Pro Glu
            260
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<210> 12
<211> 260
<212> PRT
<213> Homo sapiens

<400> 12
Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr

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1               5                  10                  15

Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
            20                  25                  30

Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
        35                  40                  45

Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
    50                  55                  60

Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
65                  70                  75                  80

Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
                85                  90                  95

Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
            100                 105                 110

Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
        115                 120                 125

Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
    130                 135                 140

Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
145                 150                 155                 160

Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
                165                 170                 175

Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
            180                 185                 190

Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
        195                 200                 205

Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
    210                 215                 220

Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
225                 230                 235                 240

Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
                245                 250                 255

Ala Asp Pro Glu
            260
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<210> 13
<211> 269
<212> PRT
<213> Murinae gen. sp.

<400> 13

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Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
 1               5                  10                  15

Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
            20                  25                  30

Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
        35                  40                  45

Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
    50                  55                  60

Phe Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn Glu
65                  70                  75                  80

Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln Leu
                85                  90                  95

Ala Ala Gln Gly Glu Leu Ser Gln Leu Lys Asp His Leu Arg Lys Gly
            100                 105                 110

Ala Cys Pro Ala Cys Thr Cys Leu Ser Gly Asn Asn Leu Ile Asn Lys
        115                 120                 125

Pro Asp Glu Arg Gly Phe Thr Pro Leu Ile Trp Ala Ser Ala Phe Gly
    130                 135                 140

Glu Ile Glu Thr Val Arg Phe Leu Leu Asp Trp Gly Ala Asp Pro His
145                 150                 155                 160

Ile Leu Ala Lys Glu Arg Glu Ser Ala Leu Ser Leu Ala Ser Met Gly
                165                 170                 175

Gly Tyr Thr Asp Ile Val Arg Leu Leu Leu Asp Arg Asp Val Asp Ile
            180                 185                 190

Asn Ile Tyr Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val Arg
        195                 200                 205

Gly Asn His Val Lys Cys Val Glu Ala Leu Leu Ala Arg Gly Ala Asp
    210                 215                 220

Leu Thr Thr Glu Ala Asp Ser Gly Tyr Thr Pro Met Asp Leu Ala Val
225                 230                 235                 240
```

Ala Leu Gly Tyr Arg Lys Val Gln Gln Val Met Glu Ser His Ile Leu
245 250 255

Arg Leu Phe Gln Ser Thr Leu Gly Pro Val Asp Pro Glu
260 265

<210> 14
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(111)

<400> 14
acc cta gac tgg tgc cga ccc cca cat cct ggc aaa aga gcg aga gag 48
Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
1 5 10 15

cgc cct gtc gct ggc cag cac agg cgg cta cac aga cat tgt ggg gct 96
Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
20 25 30

gct gct gga gcg tga 111
Ala Ala Gly Ala
35

<210> 15
<211> 36
<212> PRT
<213> Homo sapiens

<400> 15
Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
1 5 10 15

Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
20 25 30

Ala Ala Gly Ala
35

<210> 16
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (31)..(42)

<400> 16
ctggtggtat tgcccgcctc ctcctgccag gtg aca acc tcg 42

<210> 17
<211> 74
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)..(27)

<400> 17
gag acc gtt cgc ttc ctg ctg gag tgg gtgcgtccca gcccagctgg 47

gcagctgggg ggttcccggg ggccttа 74

<210> 18
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (31)..(159)
<223> Amino acids at positions 31, 148 and 159 are Xaa wherein
Xaa = any amino acid.

<400> 18
Asn Ala Phe Asn Val Phe Thr Phe Val Phe His Leu Ala Glu Cys Asn
1 5 10 15

Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val Xaa Thr
20 25 30

Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
35 40 45

Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
50 55 60

Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
65 70 75 80

```
Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
                 85                  90                  95

Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
            100                 105                 110

Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
        115                 120                 125

Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
    130                 135                 140

Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr
145                 150                 155                 160

Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
                165                 170                 175

Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
            180                 185                 190

Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
        195                 200                 205

Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
    210                 215                 220
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<210> 19
<211> 218
<212> PRT
<213> Murinae gen. sp.

<400> 19

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Ala Ser Val Leu Phe Lys Ala Glu Cys Asn Ile His Thr Ser Pro Ser
  1               5                  10                  15

Pro Gly Ile Gln Val Arg His Val Tyr Thr Pro Ser Thr Thr Lys His
             20                  25                  30

Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu Thr Asn Lys His Arg Gly
         35                  40                  45

Asn Glu Val Ser Thr Thr Pro Leu Leu Ala Asn Ser Leu Ser Ala His
     50                  55                  60

Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr Leu Ala Thr Arg Ile Glu
 65                  70                  75                  80

Gln Glu Asn Val Ile Asn His Thr Asp Glu Glu Gly Phe Thr Pro Leu
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85 90 95

Met Trp Ala Ala Ala His Gly Gln Ile Ala Val Val Glu Phe Leu Leu
100 105 110

Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly Lys Gly Arg Glu Ser Ala
115 120 125

Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr Asp Ile Val Lys Met Leu
130 135 140

Leu Asp Cys Gly Val Asp Val Asn Glu Tyr Asp Trp Asn Gly Gly Thr
145 150 155 160

Pro Leu Leu Tyr Ala Gly His Gly Asn His Val Lys Cys Val Lys Met
165 170 175

Leu Leu Glu Asn Gly Ala Asp Pro Thr Ile Glu Thr Asp Ser Gly Tyr
180 185 190

Asn Ser Met Asp Leu Ala Val Ala Leu Gly Ile Glu Gly Cys Ser Asp
195 200 205

Tyr Met Leu Val Thr Asp Val Phe Arg Ile
210 215

<210> 20
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FLAG epitope

<400> 20

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 21
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DRA promoter template

<400> 21

ggacccttg caag 14

<210> 22
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DRA promoter template

<400> 22
tacatagcgt acgt 14